SEQUENCE LISTING

<110> Better, Marc D.
Horwitz, Arnold H.

<120> Human Engineered to Antibodies to Ep-CAM

<130> 14923US02

<150> 60/459,334
<151> 2003-03-31

<160> 59

<170> PatentIn version 3.2

<210> 1
<211> 720
<212> DNA
<213> Homo Sapiens

<220>
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<223> Mouse Human Chimeric Light Chain DNA and Protein

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Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                 -5

gga tcc act gca gat att gtg atg acg cag gct gca ttc tcc aat cca       96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
           -1  1                5                  10

gtc act ctt gga aca tca ggt tcc atc tcc tgc agg tct agt aag agt      144
Val Thr Leu Gly Thr Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aag      192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

cca ggc cag tct cct cag ctc ctg att tat cag atg tcc aac ctt gcc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
45                  50                  55                  60
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tca gga gtc cca gac agg ttc agt agc agt ggg tca gga act gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

aca ctg aga atc agc aga gtg gag gct gag gat gtg ggt gtt tat tac      336
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

tgt gct caa aat cta gaa ctt cct cgg acg ttc ggt gga ggc acc aag      384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys
        95                  100                 105

ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag      720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
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<210> 2
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<212> PRT
<213> Homo Sapiens

<400> 2

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Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
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            -1  1               5                   10

Val Thr Leu Gly Thr Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
45                  50                  55                  60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys
        95                  100                 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
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<210> 3
<211> 1398
<212> DNA
<213> Homo Sapiens

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Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
                -15                 -10                 -5

gcc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag       96
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
        -1  1               5                   10

cct gga gag aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc      144
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
    15                  20                  25

aca aaa tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta      192
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
30                  35                  40                  45

aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt      240
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
                50                  55                  60

gat gac ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc      288
Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
            65                  70                  75

act gcc aat ttg cag atc aac aac ctc aaa agt gag gac acg gct aca      336
Thr Ala Asn Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Thr Ala Thr
        80                  85                  90

tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga      384
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
    95                  100                 105

acc tcg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc      432
Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
```

```
110                 115                 120                 125

ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg      480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                130                 135                 140

ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg      528
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
            145                 150                 155

aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta      576
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
        160                 165                 170

cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc      624
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
    175                 180                 185

agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc      672
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
190                 195                 200                 205

agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa      720
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
                210                 215                 220

act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg      768
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
            225                 230                 235

tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc      816
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
        240                 245                 250

cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac      864
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
    255                 260                 265

cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat      912
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
270                 275                 280                 285

gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg      960
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                290                 295                 300

gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag     1008
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
            305                 310                 315

tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa     1056
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
        320                 325                 330
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acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc     1104
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    335                 340                 345

ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc     1152
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
350                 355                 360                 365

tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag     1200
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                370                 375                 380

agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg     1248
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
            385                 390                 395

gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag     1296
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
        400                 405                 410

agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag     1344
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    415                 420                 425

gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt     1392
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
430                 435                 440                 445

aaa tga                                                            1398
Lys
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<212> PRT
<213> Homo Sapiens

<400> 4

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        -1  1               5                   10

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
    15                  20                  25

Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
30                  35                  40                  45
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Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
                50                  55                  60

Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
            65                  70                  75

Thr Ala Asn Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Thr Ala Thr
        80                  85                  90

Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
    95                  100                 105

Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
110                 115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
            145                 150                 155

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
        160                 165                 170

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
    175                 180                 185

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
190                 195                 200                 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
                210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
            225                 230                 235

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
        240                 245                 250
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```
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
    255                 260                 265

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
270                 275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
            305                 310                 315

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
        320                 325                 330

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    335                 340                 345

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
350                 355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
            385                 390                 395

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
        400                 405                 410

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    415                 420                 425

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
430                 435                 440                 445

Lys
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<210> 5
<211> 720

<212> DNA
<213> Homo Sapiens

<220>
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<223> Low Risk Human Engineered ING-1 Light Chain (LC)

<220>
<221> misc_feature
<223> Variable Region of the Light Chain is Amino Acids 1-112

<220>
<221> CDS
<222> (1)..(717)

<220>
<221> mat_peptide
<222> (61)..()

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atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct       48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                 -5

gga tcc act gca gac atc gtg atg acc cag tct gca ctc tcc aat cca       96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
            -1  1               5                   10

gtc act ctg gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt      144
Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag      384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
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Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag      720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
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<210> 6
<211> 239
<212> PRT
<213> Homo Sapiens

<400> 6

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Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
            -1  1               5                   10

Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60
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```
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
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<210> 7
<211> 720
<212> DNA
<213> Homo Sapiens

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<223> Low + Moderate Risk Human Engineered ING-1 Light Chain (LC)

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<222> (1)..(717)

<220>
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<222> (61)..()

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-20                 -15                 -10                 -5

gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc ctg cca       96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
            -1  1                5                  10

gtc act cct gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt      144
Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

tgt gct cag aac cta gag ctt cca cgg acg ttc ggt cag ggc acc aag      384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170
```

```
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag      720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
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<210> 8
<211> 239
<212> PRT
<213> Homo Sapiens

<400> 8

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-20                 -15                 -10                 -5

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
            -1  1               5                   10

Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120
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Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125 130 135 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
160 165 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
175 180 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
190 195 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210 215

<210> 9
<211> 88
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> KL1 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

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atccactgca gacatcgtga tgacccag 88

<210> 10
<211> 85
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> KL2 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

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tgcagactgg gtcatcacga tgtct 85

<210> 11
<211> 88
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> KL3 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

<400> 11
ctgccggtct agtaagagtc tcctacatag taatggcatc acttatttgt attggtatct 60

gcagaaacca gggcagtctc ctcagctg 88

<210> 12
<211> 86
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> KL4 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

<400> 12
tgtcccagat ccactgctac tgaacctgtc tgggacccct gaggctctgt tagacatctg 60

atagatgagc agctgaggag actgcc 86

<210> 13
<211> 77
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> KL5 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

<400> 13
agcagtggat ctgggacaga tttcactctc aagatcagca gagtggaggc tgaagatgtg 60

ggagtttatt actgtgc 77

<210> 14
<211> 75
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> KL6 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

<400> 14
tttgatttca agcttggtgc cctgaccgaa cgtccgtgga agctctaggt tctgagcaca 60

gtaataaact cccac 75

<210> 15
<211> 22
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> Low Risk Primers Forward Primer: KF ING-1 Light Chain Oligos

<400> 15
ttatgtcgac accatgaggt tc 22

<210> 16
<211> 21
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> Low risk Primers Reverse Primer: KR ING-1 Light Chain Oligos

<400> 16
tttgatttca agcttggtgc c 21

<210> 17
<211> 85
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> Moderate Risk Primer: KM2 V Region Oligos Human Engineered ING-1 Light Chain Oligos (Kappa Moderate)

<400> 17
actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gcagggagag 60

tggagactgg gtcatcacga tgtct 85

<210> 18
<211> 1398
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> Low Risk Human Engineered ING-1 Heavy Chain (HC)

<220>
<221> misc_feature
<223> Variable region of HC is Amino Acids is 1-116

<220>
<221> CDS
<222> (1)..(1395)

<220>
<221> mat_peptide
<222> (58)..()

<400> 18
atg gct tgg gtg tcc acc ttg cta ttc ctg atg gca gct gcc caa agt 48
Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
-15 -10 -5

gcc caa gca cag atc cag ttg gtg cag tct gga cct gag gtg aag aag 96
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
-1 1 5 10

cct gga gag tcc gtc aag atc tcc tgc aag gct tct gga tat acc ttc 144
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25

aca aaa tat gga atg aac tgg gtg aag cag gct cca gga cag ggt tta 192
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
30 35 40 45

aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt 240
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
50 55 60

```
gat gac ttc aag gga cgg ttt acc ttc acc ttg gac acc tct act agc      288
Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
            65                  70                  75

act gcc tat ttg gaa atc tct tct ctc cgg agt gag gac acg gct aca      336
Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr
        80                  85                  90

tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga      384
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
    95                  100                 105

acc ttg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc      432
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
110                 115                 120                 125

ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg      480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                130                 135                 140

ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg      528
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
            145                 150                 155

aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta      576
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
        160                 165                 170

cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc      624
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
    175                 180                 185

agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc      672
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
190                 195                 200                 205

agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa      720
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
                210                 215                 220

act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg      768
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
            225                 230                 235

tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc      816
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
        240                 245                 250

cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac      864
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
    255                 260                 265

cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat      912
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
```

```
270                 275                 280                 285

gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg      960
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                290                 295                 300

gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag     1008
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
            305                 310                 315

tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa     1056
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
        320                 325                 330

acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc     1104
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    335                 340                 345

ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc     1152
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
350                 355                 360                 365

tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag     1200
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                370                 375                 380

agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg     1248
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
            385                 390                 395

gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag     1296
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
        400                 405                 410

agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag     1344
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    415                 420                 425

gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt     1392
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
430                 435                 440                 445

aaa tga                                                            1398
Lys
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<210> 19
<211> 465
<212> PRT
<213> Homo Sapiens

<400> 19

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Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
               -15                 -10                  -5

Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
        -1  1                5                  10

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
    15                  20                  25

Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
30                  35                  40                  45

Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
                50                  55                  60

Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
            65                  70                  75

Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr
        80                  85                  90

Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
    95                  100                 105

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
110                 115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
            145                 150                 155

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
        160                 165                 170

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
    175                 180                 185

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
190                 195                 200                 205
```

```
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
                210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
            225                 230                 235

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
        240                 245                 250

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
    255                 260                 265

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
270                 275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
            305                 310                 315

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
        320                 325                 330

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    335                 340                 345

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
350                 355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
            385                 390                 395

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
        400                 405                 410
```

```
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    415                 420                 425

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
430                 435                 440                 445

Lys
```

<210> 20
<211> 1398
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> Low + Moderate Risk Human Engineered ING-1 Heavy Chain (HC)

<220>
<221> CDS
<222> (1)..(1395)

<220>
<221> mat_peptide
<222> (58)..()

<400> 20

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atg gct tgg gtg tcc acc ttg cta ttc ctg atg gca gct gcc caa agt       48
Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
                -15                 -10                 -5

gcc caa gca cag atc cag ttg gtg cag tct gga gct gag gtg aag aag       96
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
        -1  1               5                   10

cct gga gag tca gtc aag atc tcc tgc aag gct tct gga tat acc ttc      144
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
    15                  20                  25

aca aaa tat gga atg aac tgg gtg cga cag gct cca gga caa ggt tta      192
Thr Lys Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30                  35                  40                  45

gag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt      240
Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
                50                  55                  60

cag aag ttc cag gga cgg ttt acc ttc acc ttg gac acc tct act agc      288
Gln Lys Phe Gln Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
            65                  70                  75
```

```
act gcc tat ttg gaa atc tct tcg ctc cgg agt gag gac acg gct gtg      336
Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
        80                  85                  90

tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga      384
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
    95                  100                 105

acc ttg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc      432
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
110                 115                 120                 125

ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg      480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                130                 135                 140

ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg      528
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
            145                 150                 155

aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta      576
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
        160                 165                 170

cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc      624
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
    175                 180                 185

agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc      672
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
190                 195                 200                 205

agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa      720
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
                210                 215                 220

act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg      768
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
            225                 230                 235

tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc      816
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
        240                 245                 250

cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac      864
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
    255                 260                 265

cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat      912
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
270                 275                 280                 285

gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg      960
```

```
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                290                 295                 300

gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag     1008
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
            305                 310                 315

tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa     1056
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
        320                 325                 330

acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc     1104
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    335                 340                 345

ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc     1152
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
350                 355                 360                 365

tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag     1200
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                370                 375                 380

agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg     1248
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
            385                 390                 395

gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag     1296
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
        400                 405                 410

agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag     1344
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    415                 420                 425

gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt     1392
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
430                 435                 440                 445

aaa tga                                                            1398
Lys
```

<210> 21
<211> 465
<212> PRT
<213> Homo Sapiens

<400> 21

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Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
                -15                 -10                 -5
```

```
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
        -1  1               5                   10

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
    15                  20                  25

Thr Lys Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30                  35                  40                  45

Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
                50                  55                  60

Gln Lys Phe Gln Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
            65                  70                  75

Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
        80                  85                  90

Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
    95                  100                 105

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
110                 115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
            145                 150                 155

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
        160                 165                 170

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
    175                 180                 185

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
190                 195                 200                 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
```

```
                210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
            225                 230                 235

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
        240                 245                 250

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
    255                 260                 265

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
270                 275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
            305                 310                 315

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
        320                 325                 330

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    335                 340                 345

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
350                 355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
            385                 390                 395

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
        400                 405                 410

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    415                 420                 425
```

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
430 435 440 445

Lys

<210> 22
<211> 91
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GL1 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos (gamma low)

<400> 22
tgtcgacacc atggcttggg tgtccacctt gctattcctg atggcagctg cccaaagtgc 60

ccaagcacag atccagttgg tgcagtctgg a 91

<210> 23
<211> 90
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GL2 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos (gamma low)

<400> 23
atattttgtg aaggtatatc cagaagcctt gcaggagatc ttgacggact ctccaggctt 60

cttcacctca ggtccagact gcaccaactg 90

<210> 24
<211> 91
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GL3 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos (gamma low)

<400> 24
tggatatacc ttcacaaaat atggaatgaa ctgggtgaag caggctccag gacagggttt 60

aaagtggatg ggctggataa acacctacac t 91

<210> 25
<211> 90
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GL4 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos (gamma low)

<400> 25
cagtgctagt agaggtgtcc aaggtgaagg taaaccgtcc cttgaagtca tcaccatatg 60

ttggctcttc agtgtaggtg tttatccagc 90

<210> 26
<211> 90
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GL5 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos (gamma low)

<400> 26
gacacctcta ctagcactgc ctatttggaa atctcttctc tccggagtga ggacacggct 60

acatatttct gtgcaagatt tggctctgct 90

<210> 27
<211> 85
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GL6 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos (gamma low)

<400> 27
gaccgatggg ccctttgtgc tggctgagga gacggtgacc aaggttcctt gaccccagta 60

gtccacagca gagccaaatc ttgca 85

<210> 28
<211> 22
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> Human Engineered ING-1 Heavy Chain Oligos-Low Risk Primers
Forward primer:GF

<400> 28
ttatgtcgac accatggctt gg 22

<210> 29
<211> 17
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> Human Engineered ING-1 Heavy Chain Oligos Low Risk Primers
-Reverse Primer GR

<220>
<221> misc_feature
<223> ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR

<400> 29
gaccgatggg ccctttg 17

<210> 30
<211> 90
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GM2 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
+ Moderate Risk Primers

<400> 30
atattttgtg aaggtatatc cagaagcctt gcaggagatc ttgactgact ctccaggctt 60

cttcacctca gctccagact gcaccaactg 90

<210> 31
<211> 91
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GM3 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low + Moderate Risk Primers

<400> 31
tggatatacc ttcacaaaat atggaatgaa ctgggtgcga caggctccag gacaaggttt 60

agagtggatg ggctggataa acacctacac t 91

<210> 32
<211> 90
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GM4 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low + Moderate Risk Primers

<400> 32
cagtgctagt agaggtgtcc aaggtgaagg taaaccgtcc ctggaacttc tgaccatatg 60

ttggctcttc agtgtaggtg tttatccagc 90

<210> 33
<211> 90
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GM5 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low + Moderate Risk Primers

<400> 33
gacacctcta ctagcactgc ctatttggaa atctcttcgc tccggagtga ggacacggct 60

gtgtatttct gtgcaagatt tggctctgct 90

<210> 34
<211> 720
<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<223> P1=P Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1)

<220>
<221> CDS
<222> (1)..(717)

<220>
<221> mat_peptide
<222> (61)..()

<400> 34

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atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct       48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                 -5

gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca       96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
            -1  1               5                   10

gtc act ctg gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt      144
Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag      384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
```

```
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag      720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
```

<210> 35
<211> 239
<212> PRT
<213> Homo sapiens

<400> 35

```
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                 -5

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
            -1  1               5                   10

Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75
```

```
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
```

<210> 36
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> P2=P Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 15 (P2)

<220>
<221> CDS
<222> (1)..(717)

<220>
<221> mat_peptide

<222> (61)..()

<400> 36

```
atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct       48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                 -5

gga tcc act gca gac atc gtg atg acc cag tct gca ctc tcc aat cca       96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
            -1  1               5                   10

gtc act cct gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt      144
Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag      384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185
```

```
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag      720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
```

<210> 37
<211> 239
<212> PRT
<213> Homo sapiens

<400> 37

```
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                 -5

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
            -1  1               5                   10

Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
    15                  20                  25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
30                  35                  40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
110                 115                 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
```

```
125                 130                 135                 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
```

<210> 38
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> P3=P Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 18 (P3)

<220>
<221> CDS
<222> (1)..(717)

<220>
<221> mat_peptide
<222> (61)..()

<400> 38

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atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct       48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                 -5

gga tcc act gca gac atc gtg atg acc cag tct gca ctc tcc aat cca       96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
            -1  1               5                   10

gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt      144
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25
```

```
ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag      384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag      720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
```

<210> 39
<211> 239
<212> PRT
<213> Homo sapiens

<400> 39

```
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                  -5

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
            -1  1               5                  10

Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185
```

```
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215

<210>  40
<211>  720
<212>  DNA
<213>  Homo sapiens

<220>
<221>  misc_feature
<223>  P1P2=Human Engineered (low risk) ING1 light Chain with one
       moderate risk proline change; proline at position 8 (P1) 15(P2)

<220>
<221>  CDS
<222>  (1)..(717)

<220>
<221>  mat_peptide
<222>  (61)..()

<400>  40
atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct       48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                 -5

gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca       96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
            -1  1               5                   10

gtc act cct gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt      144
Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15              20                  25

ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac      336
```

```
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag      384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag      720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
```

<210> 41
<211> 239
<212> PRT
<213> Homo sapiens

<400> 41

```
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                 -5

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
            -1  1               5                   10

Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25
```

```
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
```

<210> 42
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> P1P3= Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1) 18 (P3)

<220>
<221> CDS
<222> (1)..(717)

<220>
<221> mat_peptide
<222> (61)..()

<400> 42

```
atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct       48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                 -5

gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca       96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
            -1  1               5                   10

gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt      144
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag      384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140
```

```
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag      720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
```

<210> 43
<211> 239
<212> PRT
<213> Homo sapiens

<400> 43

```
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                 -5

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
            -1  1               5                   10

Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
```

```
            80                  85                  90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
```

<210> 44
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> P2P3=Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1) 18 (P3)

<220>
<221> CDS
<222> (1)..(717)

<220>
<221> mat_peptide
<222> (61)..()

<400> 44

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atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct       48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                 -5

gga tcc act gca gac atc gtg atg acc cag tct gca ctc tcc aat cca       96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
            -1  1               5                  10

gtc act cct gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt      144
Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag      384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140

ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                145                 150                 155

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            160                 165                 170

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        175                 180                 185

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag      672
```

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Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    190                 195                 200

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag      720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210                 215
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<210> 45
<211> 239
<212> PRT
<213> Homo sapiens

<400> 45

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Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                 -15                 -10                 -5

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
            -1  1               5                   10

Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15                  20                  25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30                  35                  40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                  50                  55                  60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110                 115                 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                 130                 135                 140
```

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
160 165 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
175 180 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
190 195 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210 215

<210> 46
<211> 85
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> P1 Oligo Human Engineered ING-1 with proline oligos

<400> 46
actcttacta gaccggcagg agatggaacc tgactctccc agagtgactg gattggagag 60

tggagactgg gtcatcacga tgtct 85

<210> 47
<211> 85
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> P2 Oligo Human Engineered ING-1 with proline oligos

<400> 47
actcttacta gaccggcagg agatggaacc tgactctcca ggagtgactg gattggagag 60

tgcagactgg gtcatcacga tgtct 85

<210> 48

<211> 85
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> P3 Oligo Human Engineered ING-1 with proline oligos

<400> 48
actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag 60

tgcagactgg gtcatcacga tgtct 85

<210> 49
<211> 85
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> P1P2 Oligo Human Engineered ING-1 with proline oligos

<400> 49
actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gattggagag 60

tgcagactgg gtcatcacga tgtct 85

<210> 50
<211> 85
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> P1P3 Oligo Human Engineered ING-1 with proline oligos

<400> 50
actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag 60

tggagactgg gtcatcacga tgtct 85

<210> 51
<211> 85
<212> DNA
<213> Homo Sapiens

<220>

<221> misc_feature
<223> P2P3 Oligo Human Engineered ING-1 with proline oligos

<400> 51
actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gattggagag 60

tgcagactgg gtcatcacga tgtct 85

<210> 52
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> Reverse Primer KBsr ING-1 Light Chain

<400> 52
cttactagac cggcaggag 19

<210> 53
<211> 798
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> EpCam truncated sequence

<220>
<221> CDS
<222> (1)..(795)

<400> 53
atg gcg ccc ccg cag gtc ctc gcg ttc ggg ctt ctg ctt gcc gcg gcg 48
Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
1 5 10 15

acg gcg act ttt gcc gca gct cag gaa gaa tgt gtc tgt gaa aac tac 96
Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
20 25 30

aag ctg gcc gta aac tgc ttt gtg aat aat aat cgt caa tgc cag tgt 144
Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
35 40 45

act tca gtt ggt gca caa aat act gtc att tgc tca aag ctg gct gcc 192
Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
50 55 60

```
aaa tgt ttg gtg atg aag gca gaa atg aat ggc tca aaa ctt ggg aga      240
Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65                  70                  75                  80

aga gca aaa cct gaa ggg gcc ctc cag aac aat gat ggg ctt tat gat      288
Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
                85                  90                  95

cct gac tgc gat gag agc ggg ctc ttt aag gcc aag cag tgc aac ggc      336
Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
            100                 105                 110

acc tcc acg tgc tgg tgt gtg aac act gct ggg gtc aga aga aca gac      384
Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
        115                 120                 125

aag gac act gaa ata acc tgc tct gag cga gtg aga acc tac tgg atc      432
Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
    130                 135                 140

atc att gaa cta aaa cac aaa gca aga gaa aaa cct tat gat agt aaa      480
Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145                 150                 155                 160

agt ttg cgg act gca ctt cag aag gag atc aca acg cgt tat caa ctg      528
Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
                165                 170                 175

gat cca aaa ttt atc acg agt att ttg tat gag aat aat gtt atc act      576
Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
            180                 185                 190

att gat ctg gtt caa aat tct tct caa aaa act cag aat gat gtg gac      624
Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
        195                 200                 205

ata gct gat gtg gct tat tat ttt gaa aaa gat gtt aaa ggt gaa tcc      672
Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
    210                 215                 220

ttg ttt cat tct aag aaa atg gac ctg aca gta aat ggg gaa caa ctg      720
Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
225                 230                 235                 240

gat ctg gat cct ggt caa act tta att tat tat gtt gat gaa aaa gca      768
Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
                245                 250                 255

cct gaa ttc tca atg cag ggt cta aaa taa                             798
Pro Glu Phe Ser Met Gln Gly Leu Lys
            260                 265
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<210> 54

<211> 265
<212> PRT
<213> Homo sapiens

<400> 54

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Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
1               5                  10                  15

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
            20                  25                  30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
        35                  40                  45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
    50                  55                  60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65                  70                  75                  80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
                85                  90                  95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
            100                 105                 110

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
        115                 120                 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
    130                 135                 140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145                 150                 155                 160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
                165                 170                 175

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
            180                 185                 190
```

```
Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
        195                 200                 205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
    210                 215                 220

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
225                 230                 235                 240

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
                245                 250                 255

Pro Glu Phe Ser Met Gln Gly Leu Lys
            260                 265
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<210> 55
<211> 945
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Full-Length EpCam

<220>
<221> CDS
<222> (1)..(942)

<220>
<221> mat_peptide
<222> (70)..()

<400> 55

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atg gcg ccc ccg cag gtc ctc gcg ttc ggg ctt ctg ctt gcc gcg gcg       48
Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
            -20                 -15                 -10

acg gcg act ttt gcc gca gct cag gaa gaa tgt gtc tgt gaa aac tac       96
Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
        -5              -1  1               5

aag ctg gcc gta aac tgc ttt gtg aat aat aat cgt caa tgc cag tgt      144
Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
10                  15                  20                  25

act tca gtt ggt gca caa aat act gtc att tgc tca aag ctg gct gcc      192
Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
                30                  35                  40
```

```
aaa tgt ttg gtg atg aag gca gaa atg aat ggc tca aaa ctt ggg aga      240
Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
            45                  50                  55

aga gca aaa cct gaa ggg gcc ctc cag aac aat gat ggg ctt tat gat      288
Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
        60                  65                  70

cct gac tgc gat gag agc ggg ctc ttt aag gcc aag cag tgc aac ggc      336
Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
    75                  80                  85

acc tcc acg tgc tgg tgt gtg aac act gct ggg gtc aga aga aca gac      384
Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
90                  95                  100                 105

aag gac act gaa ata acc tgc tct gag cga gtg aga acc tac tgg atc      432
Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
                110                 115                 120

atc att gaa cta aaa cac aaa gca aga gaa aaa cct tat gat agt aaa      480
Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
            125                 130                 135

agt ttg cgg act gca ctt cag aag gag atc aca acg cgt tat caa ctg      528
Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
        140                 145                 150

gat cca aaa ttt atc acg agt att ttg tat gag aat aat gtt atc act      576
Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
    155                 160                 165

att gat ctg gtt caa aat tct tct caa aaa act cag aat gat gtg gac      624
Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
170                 175                 180                 185

ata gct gat gtg gct tat tat ttt gaa aaa gat gtt aaa ggt gaa tcc      672
Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
                190                 195                 200

ttg ttt cat tct aag aaa atg gac ctg aca gta aat ggg gaa caa ctg      720
Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
            205                 210                 215

gat ctg gat cct ggt caa act tta att tat tat gtt gat gaa aaa gca      768
Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
        220                 225                 230

cct gaa ttc tca atg cag ggt cta aaa gct ggt gtt att gct gtt att      816
Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
    235                 240                 245

gtg gtt gtg gtg ata gca gtt gtt gct gga att gtt gtg ctg gtt att      864
```

```
Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
250                 255                 260                 265

tcc aga aag aag aga atg gca aag tat gag aag gct gag ata aag gag      912
Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
                270                 275                 280

atg ggt gag atg cat agg gaa ctc aat gca taa                          945
Met Gly Glu Met His Arg Glu Leu Asn Ala
            285                 290
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<210> 56
<211> 314
<212> PRT
<213> Homo sapiens

<400> 56

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Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
            -20                 -15                 -10

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
        -5              -1  1               5

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
10                  15                  20                  25

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
                30                  35                  40

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
            45                  50                  55

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
        60                  65                  70

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
    75                  80                  85

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
90                  95                  100                 105

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
                110                 115                 120
```

```
Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
            125                 130                 135

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
        140                 145                 150

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
    155                 160                 165

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
170                 175                 180                 185

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
                190                 195                 200

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
            205                 210                 215

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
        220                 225                 230

Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
    235                 240                 245

Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
250                 255                 260                 265

Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
                270                 275                 280

Met Gly Glu Met His Arg Glu Leu Asn Ala
            285                 290
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<210> 57
<211> 26
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Forward Primer (for both soluble and full length Ep-CAM): EC-1

<400> 57
ttatgtcgac agcatggcgc ccccgc 26

<210> 58
<211> 31
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Ep-CAM Reverse Primer (for soluble Ep-CAM): EC-2

<400> 58
gagttacgtc ccagatttta ttgggccccc t 31

<210> 59
<211> 30
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Ep-CAM Reverse Primer (for full-length Ep-CAM): EC-3

<400> 59
gtatcccttg agttacgtat tgagctcgtt 30